

Figure 1

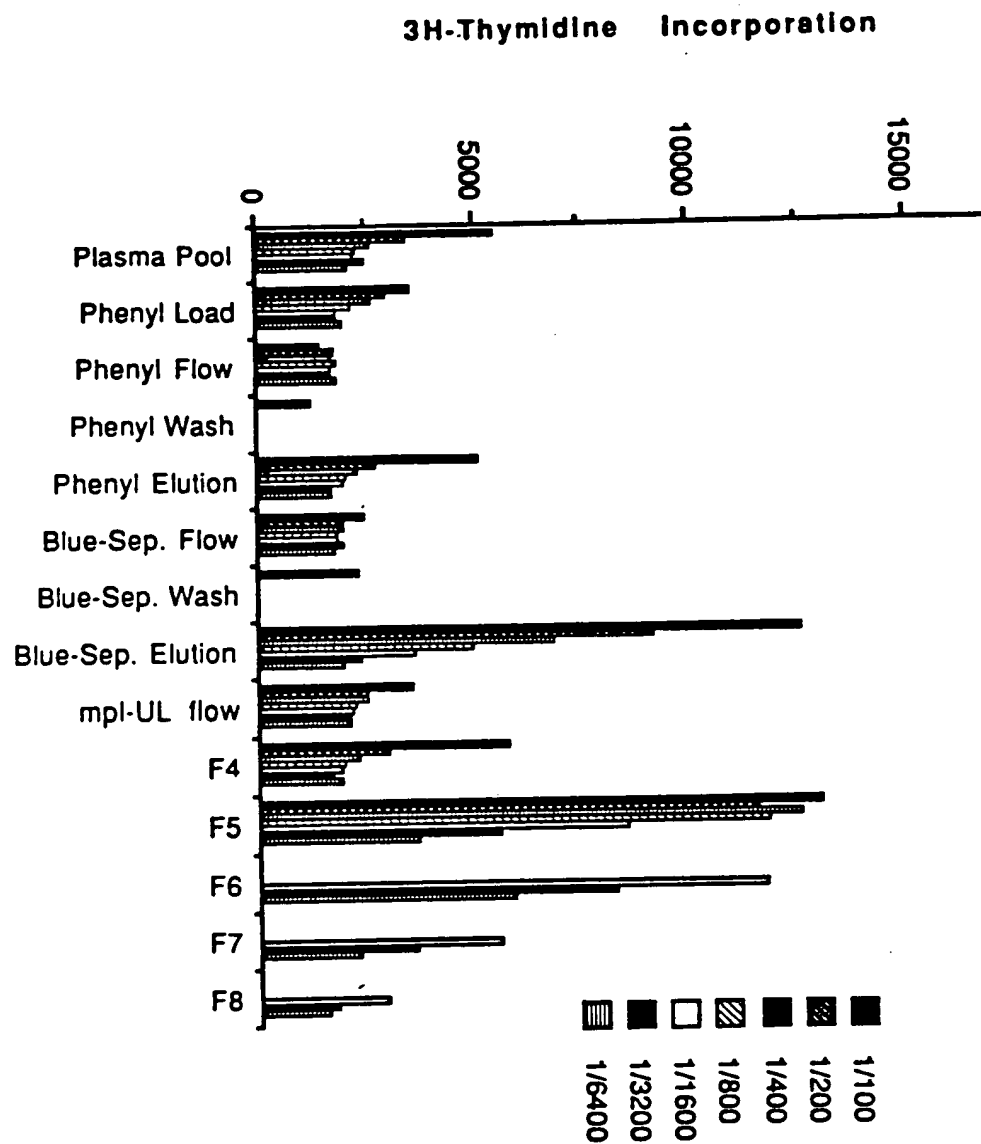
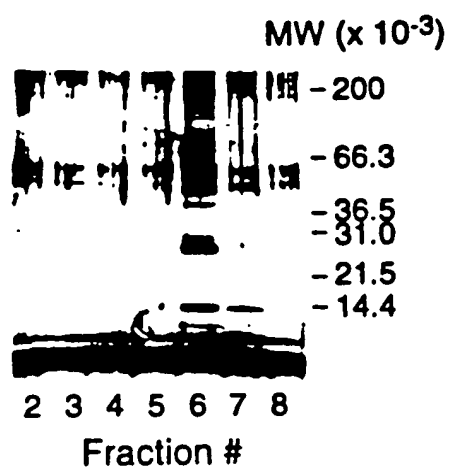


Figure 2

**Figure 3**

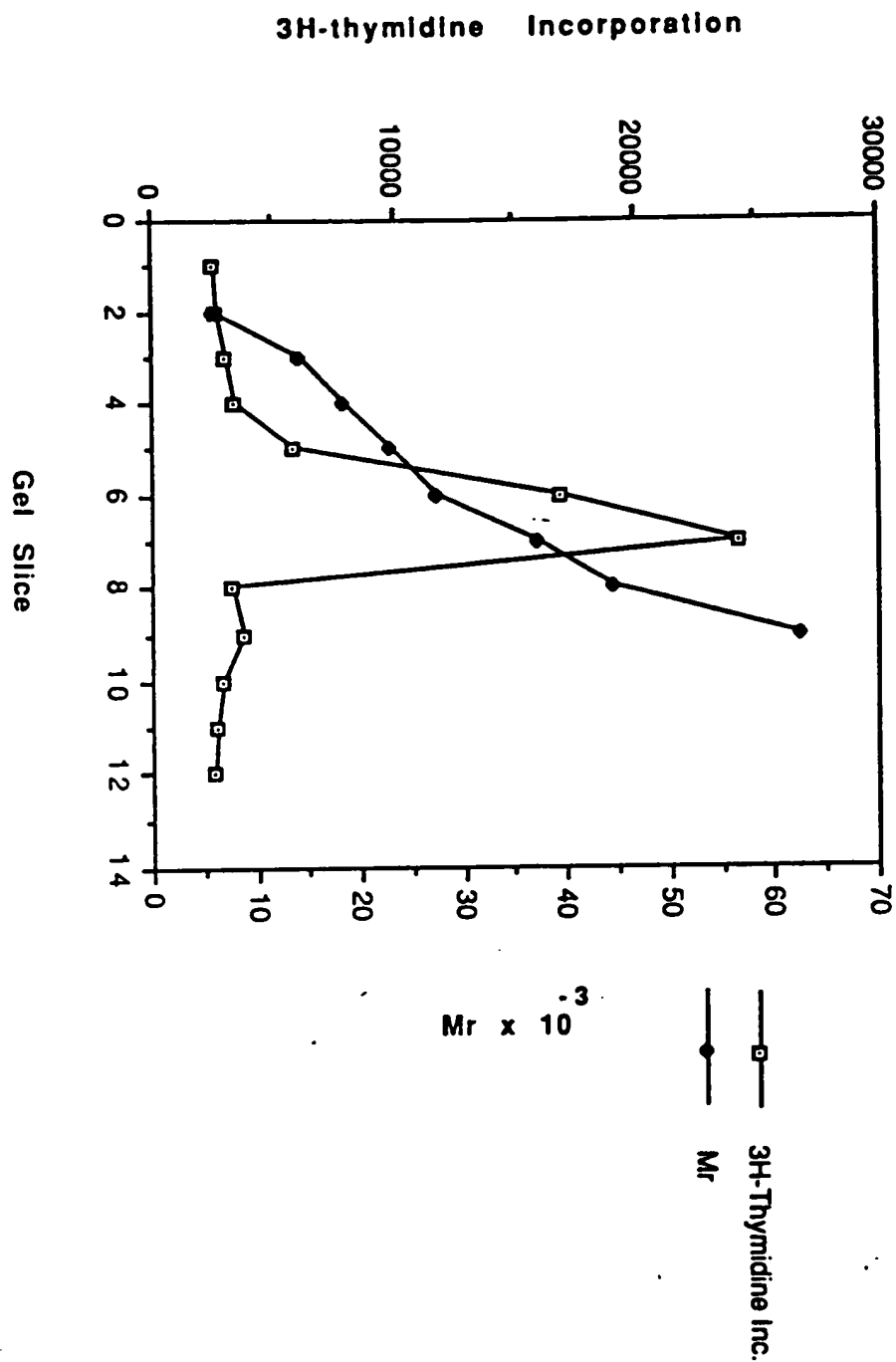


Figure 4

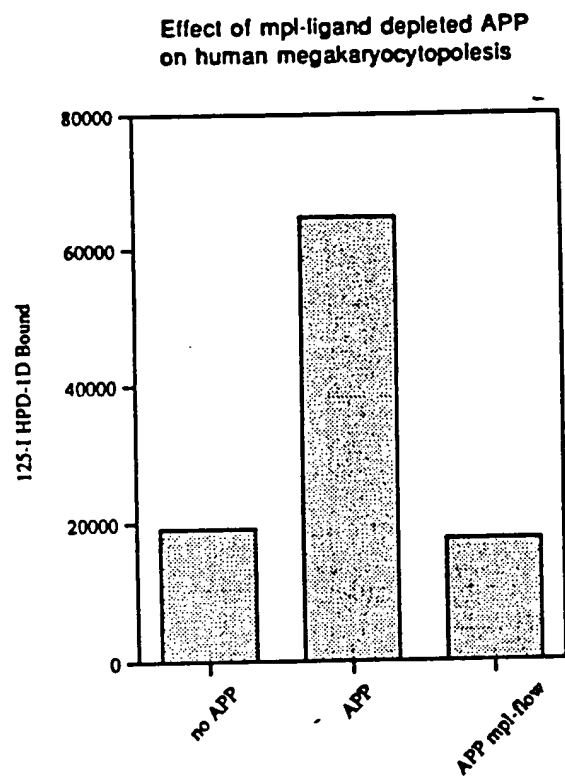


Figure 5

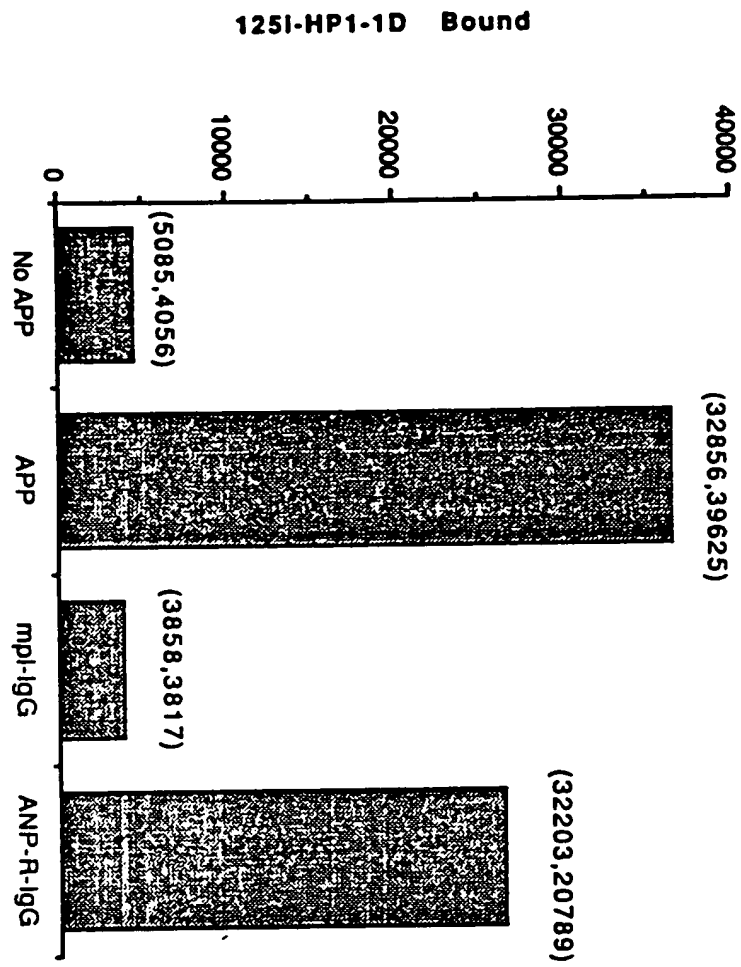


Figure 6

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 CTTAAGGACC TTATGGTCTGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGAGAGGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA
 L L L L V V M L L L T
 L L L L V V M L L L T
 101 GCAAGGCTAA CGCTGTCCAG CCGGCTCCT CCTGCTGTG ACCTCCGACT CCTCAGTAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
 CGTTCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTGC TCTGACCACT
 A R L T L S S P A P P A C D L R V L S K L L R D S H V L H S R L
 201 GAACTCCCAA CATTATCCCC TTTATCCGG TAACTGGTAA GACACCCATA CTCCGAGGAA GACACCATCA CTTCTCTTAA CTCCTTGACC CAATGACTAT
 CTTGAGGCTT GTAATAGGGG AATAGGCGC ATTGACCATT CTGTGGGTAT GAGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAAGTGG GTTACTGATA
 301 TCTTCCCATTA TTGTCCCCAC CTAATCATCA CACTCTCTGA CAAGAATTAT TCTTCACAAAT ACAGCCCGCA TTTAAAGCT CTCGTCTAGA
 AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCCGGCGT AAATTTTCCA GAGCAGATCT

Figure 7

1 ttttctaccatctgtctccccagagggtcctgctgtgacattgggtcttggagcccttctccaccggatagattcctcacttggccgccttgg

101 cccaccctactctgccagaagtgaagagcctaagccgctccatggccccaggaaggattcaggggagaggcccaaacaggagccacgccagcca

MetGluLeuThrGluLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp

201 gacaccccgccagaaTGGAGCTGACTGAATTGCTCTCGTGGTCATGCTTCTCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCTCTCTGCTTGTG

LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu

301 ACCTCCGAGTCTCAGTAAACTGCTTCTGTGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGCCAGAGGTTACCCCTTTGCTTACACTGTCTCTGTCT

ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal

401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCCTTCTGCTGGAGGGAGTG

MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu

501 ATGGCAGCACGGGACAACCTGGGACCCACTTGCCTCTCATCCTCTGGGGCAGCTTCTGGACAGGTCCGCTCTCTCTTGGGGCCCTGCAGAGCCTCC

GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe

601 TTGGAACCCAGCTTCTCTCCACAGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT

LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu

701 CCTGATGCTTGTAGGAGGGTCCACCTCTGCGTCAGGCGGGCCCCACCCACCACAGCTGTCCCCAGCAGAACCTCTCTAGTCTCACACTGAACGAGCTC

ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle

801 CCAACAGGACTTCTGGATTGTTGGAGACAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTGAGAGCCAAGA

ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro

901 TTCTCGTCTGCTGAACCAACCTCCAGGTCCCTGGACCAATCCCCGGATACCTGAACAGGATACACGAACCTTGAATGGAACCTCGTGGACTCTTTCC

GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer

1001 TGGACCTTCACGCAGGACCTTAGGAGCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCAACCTCCAGCCTGGATATTCTCTTCC

ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla

1101 CCAACCATCTCTCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCAACCTGTGGTCCAGTCCACCCCTGCTTCTGACCTTCTG

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1201 CTCCAACGCCCCACCTTACCAGCCCTCTTCTAAACACATCTACACCCACTCCCAAGATCTGTCTCAGGAAGGGTAAGgttctcagacactgccgacatc

agcattgtctcatgtacagctcccttccctgcaggcgcccttgggagacaactggacaagatttctcactttctcctgaaacccaagccctggtaaaa

1301 gggatcacaggactgaaaagggaatcatttttctactgtacattataaaccttcagaagctatttttttaagctatcagcaatctcatcagagcagcta

gtctctttgggtctatttttctgcagaaatttgcaactcactgattctctacatgtcttttttctgtgataactctgcaaaggcctgggctggcctggcagtt

1401 gaacagagggagagactaaccttgagtcagaaaaacagagaagggttaatttcttctgcttcaaattcaaggccttccaacgccccatcccccttactat

cattctcagtgaggactctgatcccatattcttaacagatctttactcttgagaaatgaataagccttctctcagaaaaa

1501

1601

1701

Figure 8

h-ML	1	S	P	A	P	A	C	D	L	R	V	L	S	K	L	R	D	S	H	V	L	H	S	R	L	S	Q	C	P	E	V	H	P	L	P	T	P	V	L	L	P	A	V	D	F	S	L	G	E	
h-epo	1	A	P	P	R	L	I	C	D	S	R	V	L	E	R	Y	L	E	A	K	E	A	E	N	I	T	T	G	C	A	E	H	C	S	L	N	E	N	I	T	V	P	D	T	K	V	N	F	Y	A
h-ML	51	W	K	T	O	M	E	E	T	K	A	O	D	I	L	G	A	V	T	L	L	E	G	V	M	A	A	R	G	O	L	G	P	T	C	L	S	-	-	S	L	L	G	O	L	S	G	O	V	R
h-epo	51	W	K	R	M	E	V	G	O	O	A	V	E	V	M	O	G	L	A	L	L	E	A	V	L	R	G	O	A	L	L	V	N	S	S	O	P	W	E	P	L	O	L	H	V	D	K	A	V	
h-ML	99	L	L	-	-	L	G	A	L	Q	S	L	L	G	T	O	-	-	L	P	Q	G	R	T	T	A	H	K	D	P	N	A	I	F	L	S	F	Q	H	L	L	R	G	K	V	R	F	L		
h-epo	101	G	L	R	S	L	T	T	L	L	R	A	L	G	A	O	K	E	A	I	S	P	P	D	A	A	S	A	P	L	R	T	I	T	A	D	T	F	R	K	L	F	R	V	Y	S	N	F	L	
h-ML	143	-	-	M	L	V	G	G	S	T	L	C	V	R	R	A	P	P	T	T	A	V	P	S	R	T	S	L	V	L	T	L	N	E	L	P	N	R	T	S	G	L	L	E	T	N	F	T	A	S
h-epo	151	G	K	L	K	L	Y	T	G	E	A	C	R	T	G	D	R																																	
h-ML	191	R	T	T	G	S	G	L	L	K	W	O	O	G	F	R	A	K	I	P	G	L	L	N	O	T	S	R	S	L	D	O	I	P	G	Y	L	N	R	I	N	E	L	L	N	G	T	R	G	L
h-ML	241	P	G	P	S	R	R	T	L	G	A	P	D	I	S	S	G	T	S	D	T	G	S	L	P	P	N	L	O	P	G	Y	S	P	S	P	T	H	P	P	T	G	O	Y	T	L	F	P	L	P
h-ML	291	T	L	P	T	P	V	V	O	L	H	P	L	L	P	D	P	S	A	P	T	P	T	S	P	L	L	N	T	S	Y	T	H	S	O	N	L	S	O	E	G									

Figure 9

1 GAGTCTCTGG CCCACTCTCT TCCACCCGGA CTCTGGCGAA AGAGGACAG AGCTCAAGC GCGCTCCATG GCGCCAGGAA AGATTCCAGG GAGAGCCCC
↓
-10
101 ATACAGGGAG CCACTTCAGT TAGACACCT GCGCAGATG GAGCTCAAGC GCGCTCCATG GCGCCAGGAA AGATTCCAGG GAGAGCCCC
Met GluLeuThr sPleuLeu uAlaMet LeuLeuAlaV alAlaArgLe uThLeuSer
-20
201 AGCCCGTAG CTCTGGCTG TGACCCGAGA CTCTTAATA AACTCTGCG TGACTCCAC CTCTTCACA GCGACTGAG TCACTGTCCC GACTCCAGC
SerProVala laProAlaCy sAspProArg LeuLeuAnL yLeuLeuAr gAspSerHis LeuLeuHis erArgLeuSe rGlnCysPro AspValaAspPro
30
301 CTTTGCTAT CCTGTTCG TGCCTCTG TGCCTCTG TGCCTCTG TGCCTCTG TGCCTCTG TGCCTCTG TGCCTCTG TGCCTCTG
LeuSeril eProValLeu LeuProAlaV alAspPheSe rLeuGlyGlu TrpLeuThrG InThrGluG InSerLyAla GlnAspIleL euGlyAlaVal
60
401 GTCCCTTCTA CTGGAGGAG TGATGGGAG ACAGGACAG TTGGAAACCT CTGCTCTCT TCCCTCTCT ATCCCTCTG GAGAGCTTT CTGGGAGGT TCCCTCTCT
70
501 TTGGGGGCC TCCAGGCCCT CCTAGGAACC CAGGGCAGG CCACAGCTCA CAGGACCCC AATGCTCTT TCTTGAGCTT CCAACAACCTG CTTCCGGGA
LeuGlyAlaL euGlnGlyLe uLeuGlyThr GlnGlyArgT hrThrAlaHi sLeuAspPro AsnAlaLeuP heLeuSerLe uGlnGlnLeu LeuArGlyLyLe
120
601 AGGTGCGCTT CTGCTCTCTG CTGAGAGGTC CCACCTCTG TGTCCAGCG ACCCTGCGA CCACAGCTGT CCAAGCAGT ACTTCTCAAC TCTCCAGCT
ValArgPh eLeuLeuLeu ValGluGlyP roThrLeuCy eValArgArg ThrLeuProT hrThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
160
701 AATCAAGTTC CCAACAGGA CTCTGCGATT GTTGAGAGC AACTTCAGT TCCAGAGCAG ACTGCTGCG CCGCTGCTT TCGAGAGCT TCGAGAGTTC
AsnLyPhe ProAsnArgT hrSerGlyLe uLeuGluThr AsnPheSerV alThrAlaAr gThrAlaGly ProGlyLeuL euserArgLe uGlnGlyPhe
180
801 AGAGTCAAGA TTACTCTCTG TCACTTCTGA CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC
ArgValLyAl lThrProAl yGlnLeuAn GlnThrSerA rgSerProVa lGlnIleSer GlyThrLeuA snArgThrHi sGlyProVal AsnGlyThrHis
220
901 ATGGGCTCTT TCGTGGAGC TCACTTCTGA CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC CCGTGGAGC
GlyLeuPh eAlaGlyThr SerLeuGlnT hrLeuGluAl eSerAspIle SerProGlyA laPheAnLy sGlySerLeu AlaPheAnL euGlnGlyLy
260
1001 ACTTCTCTCT TCTCCAGCC TTGCTCTCTG TGCACACACA CCGTCTCTCT CTTCACTCTG CCGTCTCTCT CCGTCTCTCT CCGTCTCTCT CCGTCTCTCT
LeuProPro SerProSerL euAlaProAs pGlyHisThr ProPheProp roSerProAl aleuProThr ThrHisGlyS erProProG lCTCCACCCA GCTCCACCCC
300
1101 CTGTTTCTCT ACCCTTCCAC CACATGCTCT AACTCTACCG CCGCTCATCC AGTCACAATG TACCTCTATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG
LeuPheProA spProSerTh rThrMetPro AsnSerThiA laProHisPr oValThrMet TyrProHisP roArgAnLe uSerGlnGlu Thr
320
1201 GGCAGTGGCC CAGTGAGCTT CTGAGCTTC TCTGGGAGC AAGCTTCCCC AGAGGAGCTG AGAGGAGCT GCAATCTCTC CAGATGTTCCT GCTTTCACCT
1301 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG GAGCTATTTT TTTTAACTT ATCAGCAATA TTCTATCAGAG CAGCTAGCGA
1401 TCTTGTCTCT ATTTTGGTA TAAATTTGAA AATCACTAAT TCT

Figure 10

hML 1 SPAPACDLRVLSXLLRDSHVLSRLSOCPEVHPLTPVLLPAVDFSLGE
 mML 1 SPVAPACDPRLLNXLRLRDSHLHSRLSOCPDVDPLSPVLLPAVDFSLGE

hML 51 WKTQWEETXAODILGAVTLLLEGVMAARGOLGPTCLSSLLGQLSGQVRL
 mML 51 WKTQTEOSXAODILGAVSLLLEGVMAARGOLEPSCLSSLLGQLSGQVRL

hML 101 LGALQSLLQTQLPPQORTTANKDPNAIFLSFOHLLRQKVRFLMLVGGSTL
 mML 101 LGALQGLLGT. . . . QGRTTANKDPNALFLSLQOLLRQKVRFLLLVEGPTL

hML 151 CVRRAPPTTAVPSRTSLVLTTLNELPNRTSGLLETNFTASARTTGSGLLKW
 mML 147 CVRRITLPTTAVPSSTSQLTLNKFPMRTSGLLETNFSVTARTAGPGLLSR

hML 201 OGFRAKIPGLNMTSRSLDQIPGYLNRHHELLNGTRGLFPGPSRRTL
 mML 197 LOGFRVKITPGQLNMTSRSPVQISGYLNRTHGPNMGTHGLFAGTSLQTL

hML 250 APDISSGTSDTGSLPPNLOPGYSPSPTHPPTGOYTLPPLPTLPT. . . PV
 mML 247 ASDISPGAFNKGSIAFNLOGGLPPSPSLAPDGH-TFPSPSPALPTTHGSP

hML 297 VOLHPLLPDPSAPTPTPTSPLLNTSYTHSONLSOEG
 mML 296 POLHPLFPDPSYTMPNSTAPHVPVTHYHPRNLSOET

Figure 11

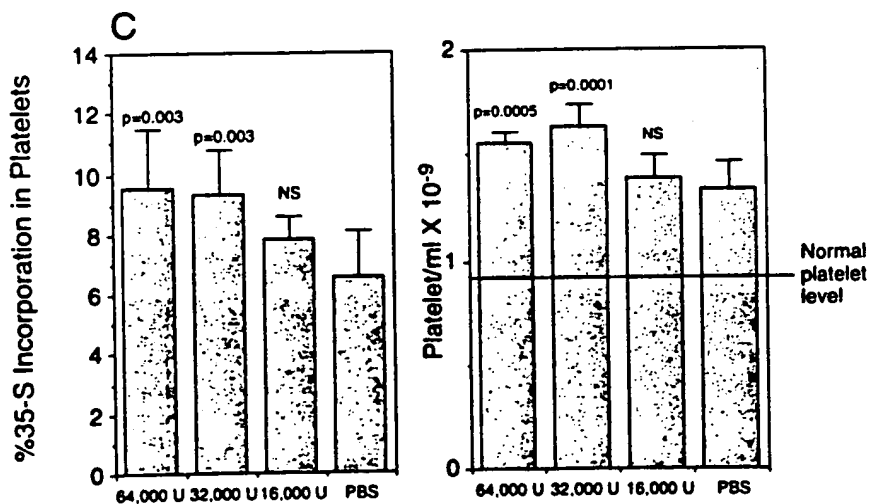
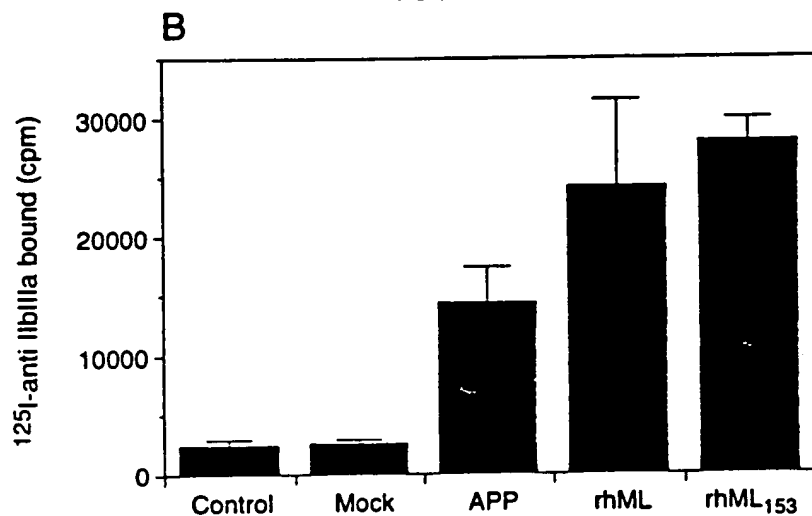
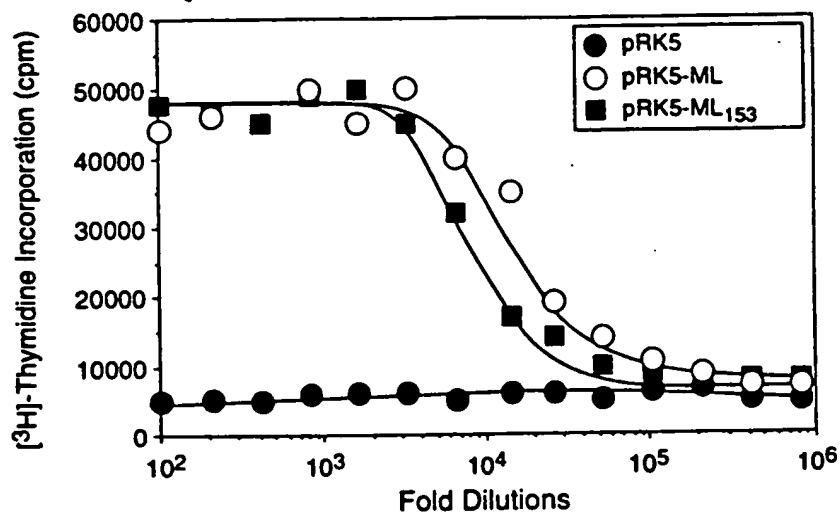


Figure 12